

2881 aggaagaacaagatgctgcaggaagaacaagatgctgctaggaagcaaatg 2940
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DB 85204 AGGAGAACAGAGCTGCGAGGAGAGAACAGAGCTGCTGCTAGGAGCAAAATG 85263
2941 aggaagatataagagattatataaagaagaagtcgcat 2979
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DB 85264 AGGAGCTATAGAGAGATTTATAGCAAGAAAGATCGTCAT 85302
|||||
RESULT 2
AP002483/c AP002483 167405 bp DNA PLN 26-JAN-2001
LOCUS Oryza sativa genomic DNA, chromosome 1, clone: P0019D06.
DEFINITION AP002483
ACCESSION AP002483
VERSION AP002483.1 GI:8468045
KEYWORDS
SOURCE Oryza sativa (cultivar: Nipponbare) DNA, clone: P0019D06.
ORGANISM Oryza sativa
Bukariyola; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae;
Oryza.
REFERENCE 1 (bases 1 to 167405)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
clone: P0019D06
JOURNAL Published only in Database (2000) In press
REFERENCE 2 (bases 1 to 167405)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2000) Takuji Sasaki, National Institute of
AUTHORS Agrobiological Resources, Rice Genome Research Program, Kannondai
TITLE 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
JOURNAL (E-mail: tsasaki@bar.affrc.go.jp, URL: http://rgrp.dna.affrc.go.jp/
COMMENT Tel: 81-298-38-7441, Fax: 81-298-38-7468)
Genes were predicted from the integrated results of the following:
GENSCAN 1.0, BLASTX 2.0, BLASTX 2.0 as well as SplicePredictor
(October 1998 version). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologues of the coding regions were searched against
NCBI NonRedundant Protein database with BLASTP 2.0. ESTs represent
the identified cDNA sequences using BLAST 2.0 with the
corresponding DB accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with EST homology (covering
almost the entire length of partial sequence) is classified as an
'unknown' protein. A gene predicted with a gene prediction program
is classified as a 'hypothetical' protein.
The orientation of the sequence is from T7 to SP6 of the PAC clone.
Detailed information on overlap and assembly quality together with
annotation of this entry is available at
http://rgrp.dna.affrc.go.jp/Genomeseq.html.
FEATURES
source
1. 167405
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7267..7644
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/note="contains EST AU062706(C30225)
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initiation codon
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TRASMAELDEEDRGYAPASRRPRHVEEETASPKKMGCIATLXIKNTYLLDONS
KLOIHEKNEHMANITLBEKEKREANSIRPAITDYLVPAGFTPQSVSDYDLEILNQLP
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